

**COMPOSITIONS AND METHODS FOR PARSING GENE STRUCTURE****ABSTRACT OF THE DISCLOSURE**

The invention provides a method for determining a sequence boundary. The method includes the steps of

- 5 (a) contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide, the target polynucleotide binding a terminal sequence of a DNA region, the addressed fragments of eukaryotic genomic DNA being at least 100 nucleotides in length; (b)
- 10 determining a relative order for 2 or more of the addressed fragments compared to a sequence of the genomic DNA; (c) identifying a pair of fragments among the 2 or more addressed fragments that alternatively bind the terminal sequence of a region; and (d) determining for
- 15 the sequence of the genomic DNA a relative location of a boundary of the region compared to a location of at least one genomic DNA fragment in the pair.